RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/583,591
Source: IFWP
Date Processed by STIC: 6/27/06

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IFWP

RAW SEQUENCE LISTING DATE: 06/27/2006
PATENT APPLICATION: **US/10/583,591** TIME: 10:43:38

Input Set : **A:\PA0394 Sequence Listing.ST25.txt**
Output Set: **N:\CRF4\06272006\J583591.raw**

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 3 <110> APPLICANT: STUBBS, Simon L.
 4       FRANCIS, Michael J.
 5       CUSHING, Adrian
 6       ISMAIL, Rahman A.
 8 <120> TITLE OF INVENTION: CYTOCHROME C PROTEIN AND ASSAY
10 <130> FILE REFERENCE: PA0394
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/583,591
13 <141> CURRENT FILING DATE: 2006-06-19
15 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/005317
16 <151> PRIOR FILING DATE: 2004-12-17
18 <150> PRIOR APPLICATION NUMBER: GB 0329353.7
19 <151> PRIOR FILING DATE: 2003-12-19
21 <160> NUMBER OF SEQ ID NOS: 15
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 315
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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33 gttgaaaagg gaggcaagca caagactggg ccaaatctcc atggtctctt tgggcggaag    120
35 acaggtcagg cccctggata ctcttacaca gccgccaata agaacaaagg catcatctgg    180
37 ggagaggata cactgatgga gtatttggag aatcccaaga agtacatccc tggaacaaaa    240
39 atgatctttg tcggcattaa gaagaaggaa gaaagggcag acttaatagc ttatctcaaa    300
41 aaagctacta atgag                                                    315
44 <210> SEQ ID NO: 2
45 <211> LENGTH: 105
46 <212> TYPE: PRT
47 <213> ORGANISM: Homo sapiens
49 <400> SEQUENCE: 2
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55 Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
56             20                  25                  30
59 Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
60         35                  40                  45
63 Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
64     50                  55                  60
67 Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro Gly Thr Lys
68 65                  70                  75                  80
71 Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
72                 85                  90                  95
75 Ala Tyr Leu Lys Lys Ala Thr Asn Glu
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79 <210> SEQ ID NO: 3
80 <211> LENGTH: 1044
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Synthetic oligonucleotide
87 <400> SEQUENCE: 3
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90 gatgttaatg ggcacaaatt ttctgtcagt ggagagggtg aaggtgatgc aacatacgga    120
92 aaacttaccc ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt    180
94 gtcactactc tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg    240
96 catgactttt tcaagagtgc catgcccgaa ggttatgtac aggaaagaac tatatttttc    300
98 aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttgtt    360
100 aatagaatcg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa    420
102 ttggaataca actataactc acacaatgta tacatcatgg cagacaaaca aaagaatgga    480
104 atcaaagtta acttcaaaat tagacacaac attgaagatg gaggcgttca actagcagac    540
106 cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac    600
108 ctgtccacaa catctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt    660
110 cttggctttg taacagctgc tgggattaca catggcatgg atgaactata caaactcgag    720
112 aattcgacca tgggtgatgt tgagaaaggc aagaagattt ttattatgaa gtgttcccag    780
114 tgccacaccg ttgaaaaggg aggcaagcac aagactgggc caaatctcca tggtctcttt    840
116 gggcggaaga caggtcaggc ccctggatac tcttacacag ccgccaataa gaacaaaggc    900
118 atcatctggg gagaggatac actgatggag tatttggaga atcccgccaa gtacatccct    960
120 ggaacaaaaa tgatctttgt cggcattaag aagaaggaag aaagggcaga cttaatagct   1020
122 tatctcaaaa aagctactaa tgag                                         1044
125 <210> SEQ ID NO: 4
126 <211> LENGTH: 348
127 <212> TYPE: PRT
128 <213> ORGANISM: Artificial Sequence
130 <220> FEATURE:
131 <223> OTHER INFORMATION: Synthetic polypeptide
133 <400> SEQUENCE: 4
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136 1               5                  10                  15
139 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
140             20                  25                  30
143 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
144         35                  40                  45
147 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
148     50                  55                  60
151 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
152 65                  70                  75                  80
155 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
156                 85                  90                  95
159 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
160             100                 105                 110
163 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
164         115                 120                 125
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167 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
168     130                 135                 140
171 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
172 145                 150                 155                 160
175 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
176                 165                 170                 175
179 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180             180                 185                 190
183 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
184         195                 200                 205
187 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val
188     210                 215                 220
191 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Glu
192 225                 230                 235                 240
195 Asn Ser Thr Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met
196                 245                 250                 255
199 Lys Cys Ser Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr
200             260                 265                 270
203 Gly Pro Asn Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro
204         275                 280                 285
207 Gly Tyr Ser Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly
208     290                 295                 300
211 Glu Asp Thr Leu Met Glu Tyr Leu Glu Asn Pro Ala Lys Tyr Ile Pro
212 305                 310                 315                 320
215 Gly Thr Lys Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala
216                 325                 330                 335
219 Asp Leu Ile Ala Tyr Leu Lys Lys Ala Thr Asn Glu
220             340                 345
223 <210> SEQ ID NO: 5
224 <211> LENGTH: 1041
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: Synthetic oligonucleotide
231 <400> SEQUENCE: 5
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234 gttgaaaagg gaggcaagca caagactggg ccaaatctcc atggtctctt tgggcggaag    120
236 acaggtcagg cccctggata ctcttacaca gccgccaata agaacaaagg catcatctgg    180
238 ggagaggata cactgatgga gtatttggag aatcccgcca agtacatccc tggaacaaaa    240
240 atgatctttg tcggcattaa gaagaaggaa gaaagggcag acttaatagc ttatctcaaa    300
242 aaagctacta atgagggtcg acccgggatg agtaaaggag aagaactttt cactggagtt    360
244 gtcccaattc ttgttgaatt agatggtgat gttaatgggc acaaattttc tgtcagtgga    420
246 gagggtgaag gtgatgcaac atacggaaaa cttaccctta aatttatttg cactactgga    480
248 aaactacctg ttccatggcc aacacttgtc actactctct cttatggtgt tcaatgcttt    540
250 tcaagatacc cagatcatat gaaacggcat gacttttttca agagtgccat gcccgaaggt    600
252 tatgtacagg aaagaactat atttttcaaa gatgacggga actacaagac acgtgctgaa    660
254 gtcaagtttg aaggtgatac ccttgttaat agaatcgagt taaaaggtat tgattttaaa    720
256 gaagatggaa acattcttgg acacaaattg gaatacaact ataactcaca caatgtatac    780
258 atcatggcag acaaacaaaa gaatggaatc aaagttaact tcaaaattag acacaacatt    840
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Input Set : **A:\PA0394 Sequence Listing.ST25.txt**
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260 gaagatggag gcgttcaact agcagaccat tatcaacaaa atactccaat tggcgatggc 900
262 cctgtccttt taccagacaa ccattacctg tccacacaat ctgccctttc gaaagatccc 960
264 aacgaaaaga gagaccacat ggtccttctt ggctttgtaa cagctgctgg gattacacat 1020
266 ggcatggatg aactatacaa a 1041
269 <210> SEQ ID NO: 6
270 <211> LENGTH: 347
271 <212> TYPE: PRT
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Synthetic polypeptide
277 <400> SEQUENCE: 6
279 Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met Lys Cys Ser
280 1 5 10 15
283 Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
284 20 25 30
287 Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
288 35 40 45
291 Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
292 50 55 60
295 Leu Met Glu Tyr Leu Glu Asn Pro Ala Lys Tyr Ile Pro Gly Thr Lys
296 65 70 75 80
299 Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
300 85 90 95
303 Ala Tyr Leu Lys Lys Ala Thr Asn Glu Gly Arg Pro Gly Met Ser Lys
304 100 105 110
307 Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
308 115 120 125
311 Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
312 130 135 140
315 Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
316 145 150 155 160
319 Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser Tyr Gly
320 165 170 175
323 Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
324 180 185 190
327 Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
328 195 200 205
331 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
332 210 215 220
335 Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
336 225 230 235 240
339 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
340 245 250 255
343 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
344 260 265 270
347 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
348 275 280 285
351 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
352 290 295 300

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355 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
356 305 310 315 320
359 Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val Thr Ala Ala
360 325 330 335
363 Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
364 340 345
367 <210> SEQ ID NO: 7
368 <211> LENGTH: 1044
369 <212> TYPE: DNA
370 <213> ORGANISM: Artificial Sequence
372 <220> FEATURE:
373 <223> OTHER INFORMATION: synthetic oligonucleotide
375 <400> SEQUENCE: 7
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378 gatgttaatg ggcacaaatt ttctgtcagt ggagagggtg aaggtgatgc aacatacgga 120
380 aaacttaccc ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt 180
382 gtcactactc tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg 240
384 catgactttt tcaagagtgc catgcccgaa ggttatgtac aggaaagaac tatattttc 300
386 aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga taccctgtt 360
388 aatagaatcg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa 420
390 ttggaataca actataactc acacaatgta tacatcatgg cagacaaaca aaagaatgga 480
392 atcaaagtta acttcaaaat tagacacaac attgaagatg gaggcgttca actagcagac 540
394 cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac 600
396 ctgtccacac aatctgccct ttcgaaagat cccaacgaaa agagagacca catggtcctt 660
398 cttggctttg taacagctgc tgggattaca catggcatgg atgaactata caaactcgag 720
400 aattcgacca tgggtgatgt tgagaaaggc aagaagattt ttattatgaa gtgttcccag 780
402 tgccacaccg ttgaaaaggg aggcaagcac aagactgggc caaatctcca tggtctcttt 840
404 gggcggaaga caggtcaggc ccctggatac tcttacacag ccgccaataa gaacaaaggc 900
406 atcatctggg gagaggatac actgatggag tatttggaga atcccaagaa gtacatccct 960
408 ggaacaaaaa tgatctttgt cggcattaag aagaaggaag aaagggcaga cttaatagct 1020
410 tatctcaaaa aagctactaa tgag 1044
413 <210> SEQ ID NO: 8
414 <211> LENGTH: 348
415 <212> TYPE: PRT
416 <213> ORGANISM: Artificial Sequence
418 <220> FEATURE:
419 <223> OTHER INFORMATION: Synthetic polypeptide
421 <400> SEQUENCE: 8
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424 1 5 10 15
427 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
428 20 25 30
431 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
432 35 40 45
435 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
436 50 55 60
439 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
440 65 70 75 80
443 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

VERIFICATION SUMMARY DATE: 06/27/2006
PATENT APPLICATION: **US/10/583,591** TIME: 10:43:39

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number